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COMMONWEALTH OF AUSTRALIA

IN THE MATTER OF: Australian Patent
Application 696764 (73941/94). In the name of:
Human Genome Sciences Inc.

-and-

IN THE MATTER OF: Opposition thereto by
Ludwig Institute for Cancer Research, under
Section 59 of the Patents Act.

STATUTORY DECLARATION

I, Susan Power of Cell & Molecular Technologies, Inc., Phillipsburg, New Jersey, United States of America, declare as follows:

1. I am currently a Senior Molecular Biologist for Cell & Molecular Technologies, Phillipsburg, New Jersey. I have held this position since July, 1999. Prior to that appointment I was a post-doctorate research scientist, studying the molecular biology of retinoids and their role in limb bud development, at the University of Wisconsin, Madison, Wisconsin for two years. Prior to that appointment, I was a post-doctorate research scientist, studying the molecular biology of the transcription factor vHNF1 at the Pasteur Institute in Paris, France for four years. I received my Ph.D. in 1991 in Microbiology, from the National University of Ireland, Galway, Ireland.
2. The Patent Attorneys for Human Genome Sciences (HGS) requested that I perform the following experiments in order to determine whether the 350 amino acid form of VEGF-2 (corresponding to residues 70 to 419 of the 419 amino acid form of VEGF-2) fused in frame with a heterologous signal sequence would result in the expression and secretion of the protein from eukaryotic cells. They have also requested that all experiments that I conducted employ techniques routinely available by March, 1994. I have done this and the experiments I have conducted are described herein. Unless I state otherwise, all methods used herein were available prior to March, 1994.

3. To determine whether the 350 amino acid form of VEGF-2 could be secreted from cells when attached to a heterologous signal sequence, I transfected eukaryotic cells with expression vectors encoding the 419 amino acid form of VEGF-2, or the 350 amino acid form of VEGF-2 fused in frame with a heterologous signal sequence. I grew the transfected cells under conditions to allow the cells to express the gene products encoded by the vectors. At various time points, I collected both cell lysates and culture medium and assayed for the presence of VEGF-2, in order to determine if the cells were secreting VEGF-2. The presence of VEGF-2 in either the cell lysates or culture medium was determined by Western Blot analysis of the samples using a polyclonal antibody to VEGF-2, which recognizes both the precursor form and the processed form of VEGF-2

4. The design of the expression vectors used in the study is as follows:

419 amino acid form of VEGF-2 (followed by a STOP codon at position 420):

ATG(1) 419aa TAA(420)
VEGF-C (419 aa)

350 amino acid form of VEGF-2 linked to a heterologous signal sequence (followed by a STOP codon at position 420):

ATG ATG (70) TAA (420)
Ig k-chain leader (aa 1-21) VEGF-C (aa 22-371)

5. The nucleotide sequences encoding the 419 and the 350 amino acid forms of VEGF-2 were obtained directly from the American Type Culture Collection (ATCC). ATCC Deposit No. 97149 contains the nucleotide sequence encoding the 419 amino acid form of VEGF-2. ATCC Deposit No. 75698 contains the nucleotide sequence encoding the 350 amino acid form of VEGF-2.

2. The nucleotide sequence encoding the 419 amino acid form of VEGF-2

was engineered to be flanked by an Eco RI site at the 5' end and a Not I site at its 3' end. The second construct contained the nucleotide sequence encoding the 350 amino acid form of VEGF-2 fused in frame with a heterologous signal sequence, Ig k-chain leader signal sequence, a recognized signal sequence which was available as of March, 1994, and was engineered to contain a Bam HI site at its 5' end and a Not I site at its 3' end. The sequence of each of these constructs was confirmed to be correct and is detailed in Appendix I, attached hereto.

6. Each VEGF-2 construct was subcloned into the expression vector pCMV-I (see attached plasmid map, attached hereto as Appendix II), so that the VEGF-2 sequences were under the control of a CMV-I promoter, a promoter routinely used as of March, 1994. The 419 amino acid form of VEGF-2 was subcloned into the Eco RI/Not I sites of pCMV-I, while the 350 amino acid form of VEGF-2 fused in frame with a heterologous signal sequence, was subcloned into the Bam HI/Not I sites of pCMV-I (see plasmid map, Appendix II).
7. The two VEGF-2 constructs were transiently transfected in duplicate, using the lipofectin method, comparable methods were routinely used as of March, 1994, into the Human Embryonic Kidney cell line, HEK-293 tsA-0, a cell line which was also routinely used as of March, 1994. As a control for transfection efficiency, each construct was co-transfected with the vector pCMV- β -gal. The efficiency of transfection was determined by β -gal staining 48 hours after transfection. As a negative control the vector pCMV-I without an insert was transfected in parallel.
8. The transfection design is as follows:
 - 10 dishes transfected with: pCMV-I-VEGF-419;
 - 10 dishes transfected with: pCMV-I-signal sequence-VEGF-350;
 - 10 dishes transfected: pCMV-I;
 - 2 dishes transfected with: pCMV-I-VEGF-419 + pCMV- β -gal; and
 - 2 dishes transfected with: pCMV-I-signal sequence-VEGF-350 + pCMV- β -gal.

9. After transfection, DMEM medium containing 3% serum was added to the cells. Aliquots of cell extracts and conditioned medium were prepared from each transfection at: T_0 hours, T_{16} hours, T_{24} hours, T_{48} hours and T_{72} hours, in duplicate.
10. At the time of harvesting the cells and medium were treated as follows:
Medium: Harvested medium was concentrated 3 fold using Centricon 10 concentrator devices. One volume of 2 x PAGE loading dye was added to each sample.
Cell Extracts: The cells were harvested by trypsinization and collected by centrifugation. The cell pellet was resuspended and lysed in 250 μ l of 1x PAGE loading buffer.
11. To determine the transfection efficiency, dishes transfected with the pCMV- β -gal construct were fixed and stained for β -gal activity 48 hours after transfection. All dishes were found to have the same percentage of transfected cells (70%).
12. Each protein sample was subjected to Western analysis as outlined below. Prior to loading on to a 12% (w/v) Tris-Glycine SDS-Polyacrylamide gel, the samples were boiled for 5 minutes and cooled on ice. The two end lanes of each gel contained the appropriately sized molecular weight markers to estimate the migration rate of proteins predicted to run in the 16 to 85 kDa size range. The samples were electrophoresed according to standard conditions.
13. Following electrophoresis, the samples were transferred to a PVDF membrane. Each membrane was blocked by a one hour incubation in phosphate buffered saline (PBS) containing 3% Bovine Serum Albumin (BSA). The blot was then incubated at 4°C in PBS containing 0.1% BSA and 500ng/ul of purified rabbit anti-VEGF-2 antibody, a polyclonal antibody which recognizes the precursor form and the processed form of VEGF-2. After three 5 minute washes in PBS containing 0.1% Tween, the blot was incubated for 1 hour in PBS containing 0.1% BSA and a 1:3000 dilution of Goat Anti-Rabbit IgG

Horse Radish Peroxidase (HRP) conjugated antibody. The blot was washed three times for 5 minutes in PBS containing 0.1% BSA. The blot was developed with 2ml/blot of ECL detection reagent (obtained from Amersham) for one minute and then exposed directly to Polaroid films for approximately 5 seconds.

14. The result of the experiment is shown in Figure 1, attached hereto. The samples included in the figure are as follows:

Immunoblot analysis of VEGF derivatives transiently expressed in HEK293T cells

Lane	Pellet/Supe rn.	350aa -signal / 419aa	T (h) post-transfection
Gel 1			
1	P	419	24
2	S	419	24
3	P	350-signal	24
4	S	350-signal	24
5	P	350-signal	24
6	S	350-signal	24
7	P	negative control	24
8	S	positive control	48
Gel 2			
9	P	419	48
10	S	419	48
11	P	419	48
12	S	419	48
13	P	350-signal	48
14	S	350-signal	48

15	P	350-signal	48
16	S	350-signal	48
17	P	negative control	
18	S	negative control	
Gel 3			
19	P	419	72
20	S	419	72
21	P	419	72
22	S	419	72
23	P	350-signal	72
24	S	350-signal	72
25	S	350-signal	72
26	P	350-signal	72

15. The Western Blot analysis indicates that a doublet of approximately 30kDa was present in the medium collected from the transfection of both the 419 amino acid form of VEGF-2 and the 350 amino acid-VEGF-2 signal sequence constructs (see Figure 1). The secreted protein was visible beginning at 16 hours after transfection. The secreted product from cells containing the 419 amino acid construct and the 350 amino acid-VEGF2 signal sequence construct are approximately the same size.

AND I declare that all the statements made in this Declaration are of my own
are true in every particular, and that all statements made on information and belief are
believed to be true.

Sworn by the said Susan Power, Susan Power at
Phillipsburg, New Jersey, on this 3rd day of December 2000;
before me Maryann White
Notary Public

MARYANN WHITE
NOTARY PUBLIC, State of New York
No. 4883761
Qualified in Nassau County
Certification Filed in New York County
Commission Expires January 26, 2001

*** TOTAL PAGE.07 ***

VEGF-2 350aa +Signal Sequence:

+1 DpnI -
 +1 BamHI -
 +1 Ncol -
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu
 1 GGATCCGCCA CCATGGAGAC AGACACACTC CTGCTATGGG TACTGCTGCT
 CCTAGCGGT GGTACCTCTG TCTGTGTGAG GACGATAACCC ATGACGACGA
 +1 SspI -
 +1 Leu Trp Val Pro Gly Ser Thr Gly Asp Met Thr Val Leu Tyr Pro Glu Tyr Trp
 51 CTGGGTTCCA GTTCCACTG GTGACATGAC TGTACTCTAC CCAGAATATT
 GACCAAGGT CCAAGGTGAC CACTGTACTG ACATGAGATG GGTCTTATAA
 +1 Ddel -
 +1 Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg
 101 GGAAAATGTA CAAGTGTAG CTAAGGAAAG GAGGCTGGCA ACATAACAGA
 CCTTTTACAT GTTCACAGTC GATTCTTTC CTCCGACCGT TGTATTGTCT
 +1 PstI -
 +1 Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala
 151 GAACAGGCCA ACCTCAACTC AAGGACAGAA GAGACTATAA AATTGCTGC
 CTTGTCGGT TGGAGTTGAG TTCTGTCTT CTCTGATATT TTAAACGACG
 +1 DpnI -
 +1 PstI -
 +1 BglII -
 +1 Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
 201 AGCACATTAT AATACAGAGA TCTTGAAAAG TATTGATAAT GAGTGGAGAA
 TCGTGTAAATA TTATGTCTCT AGAACTTTTC ATAACATATTA CTCACCTCTT
 +1 SphI -
 +1 Lys Thr Gin Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
 251 AGACTCAATG CATGCCACGG GAGGTGTGTA TAGATGTGGG GAAGGAGTTT
 TCTGAGTTAC GTACGGTGCC CTCCACACAT ATCTACACCC CTTCTCTAAA
 +1 NruI -
 +1 DraI -
 +1 AccI -
 +1 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg
 301 GGAGTCGCGA CAAACACCTT CTTAACACCT CCATGTGTGT CCGTCTACAG
 CCTCAGCGCT GTTTGTGGAA GAAATTGGAA GGTACACACACA GGCAGATGTC
 +1 PstI -
 +1 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gin Cys Met Asn Thr Ser Thr
 351 ATGTGGGGGT TGCTGCAATA GTGAGGGCT GCAGTGCATG AACACCAGCA
 TACACCCCCA ACACGTTAT CACTCCCCGA CGTCACGTAC TTGTGGTCGT
 +1 Ddel -
 +1 Th Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gin
 401 CGAGCTACCT CAGCAAGACG TTATTGAAA TTACAGTGCC TCTCTCTCAA
 GCTCGATGGA GTCGTTCTGC AATAAACTTT AATGTCACCG AGAGAGAGTT
 +1 Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys
 451 GGCCCCAAC CAGTAACAAT CAGTTTGCC AATCACACTT CCTGCCGATG
 CCGGGGTTTG GTCATTGTTA GTCAAAACGG TTAGTGTGAA GGACGGCTAC
 +1 Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser
 501 CATGTCTAAA CTGGATGTTT ACAGACAAAGT TCATTCCATT ATTAGACGTT
 GTACAGATTG GACCTACAAA TGTCTGTTCA AGTAAGGTTAA TAATCTGCAA
 +1 Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro
 551 CCCTGCCAGC AACACTACCA CAGTGTCAAGG CAGCGAACAA GACCTGCCCC
 GGGACGGTCG TTGTGATGGT GTCACAGTCC GTCGCTTGTGTT CTGGACGGGG

PstI

+1 Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala Gln Glu Asp

601 ACCAATTACA TGTGGAATAA TCACATCTGC AGATGCCTGG CTCAGGAAGA
TGGTTAATGT ACACCTTATT AGTGTAGACG TCTACGGACC GAGTCCTTCT

+1 Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp Gly Phe His Asp

651 TTTTATGTTT TCCTCGGATG CTGGAGATGA CTCAACAGAT GGATTCCATG
AAAATACAAA AGGAGCCTAC GACCTCTACT GAGTTGTCTA CCTAAGGTAC

PstI

+1 Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys Val

701 ACATCTGTGG ACCAAACAAG GAGCTGGATG AAGAGACCTG TCAGTGTGTC
TGTAGACACC TGGTTGTTCTCGACCTAC TTCTCTGGAC AGTCACACAG

PvuII

+1 Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro His Lys Glu Leu Asp

751 TGCAGAGCGG GGCTTCGGCC TGCCAGCTGT GGACCCCACA AAGAACTAGA
ACGTCTCGCC CCGAAGCCGG ACGGTCGACA CCTGGGGTGT TTCTTGATCT

+1 Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys

801 CAGAAACTCA TGCCAGTGTG TCTGTAAAAA CAAACTCTTC CCCAGCCAAT
GTCTTGAGT ACGGTACAC AGACATTTTT GTTTGAGAAG GGGTCGGTTA

+1 Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys

851 GTGGGGCCAA CCGAGAATT GATGAAAACA CATGCCAGTG TGTATGTAAA
CACCCCGGTT GGCTCTTAAA CTACTTTGT GTACGGTCAC ACATACATT

+1 Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu

901 AGAACCTGCC CCAGAAATCA ACCCCTAAAT CCTGGAAAAT GTGCCTGTGA
TCTTGGACGG GGTCTTAGT TGGGGATTAA GGACCTTTA CACGGACACT

+1 Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His

951 ATGTACAGAA AGTCCACAGA AATGCTTGT AAAAGGAAAG AAGTTCCACC
TACATGTCTT TCAGGTGTCT TTACGAACAA TTTCCCTTC TTCAAGGTGG

PvuII

+1 His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala

1001 ACCAAACATG CAGCTGTTAC AGACGGCCAT GTACGAACCG CCAGAAGGCT
TGGTTGTTAC GTCGACAATG TCTGCCGGTA CATGCTTGGC GGTCTTCCGA

+1 Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser

1051 TGTGAGCCAG GATTTTCATA TAGTGAAGAA GTGTGTCGTT GTGTCCCTTC
ACACTCGGTC CTAAAAGTAT ATCACTTCTT CACACAGCAA CACAGGGAAG

DdeI

+1 Ser Tyr Trp Lys Arg Pro Gln Met Ser ***

1101 ATATTGGAAA AGACCACAAA TGAGCTAACGC GGCCGGCG
TATAACCTTT TCTGGTGTTC ACTCGATTCC CGGGCGC

VEGF-2 419aa Sequence:

EcoRI
 +1 Met His Leu Leu Gly Phe Phe Ser Val Ala
 1 GAATTCTGG GTCCTTCCAC CATGCACTTG CTGGGCTTCT TCTCTGTGGC
 CTTAAGCACC CAGGAAGGTG GTACGTGAAC GACCCGAAGA AGAGACACCG

SmaI
XmaI
AvaI
NruI
 +1 Ala Cys Ser Leu Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala
 51 GTGTTCTCTG CTCGCCGCTG CGCTGCTCCC GGGTCCTCGC GAGGCGCCCG
 CACAAGAGAC GAGCGGCGAC GCGACGAGGG CCCAGGAGCG CTCCGGGGC

+1 Ala Ala Ala Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro
 101 CCGCCGCCGC CGCCTTCGAG TCCGGACTCG ACCTCTCGGA CGCGGAGCCC
 GGCGGCGGGC GCGGAAGCTC AGGCCTGAGC TGGAGAGCCT GCGCCTCGGG

DpnI
BglII
 +1 Asp Ala Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu
 151 GACGCAGGGCG AGGCCACGGC TTATGCAAGC AAAGATCTGG AGGAGCAGTT
 CTGCGCCCGC TCCGGTGCCG AATACGTTCG TTTCTAGACC TCCTCGTCAA

SspI
 +1 Leu Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr
 201 ACGGTCTGTG TCCAGTGTAG ATGAACATCAT GACTGTACTC TACCCAGAAT
 TGCCAGACAC AGGTACACATC TACTTGAGTA CTGACATGAG ATGGGTCTTA

SspI
DdeI
 +1 Tyr Trp Lys Met Tyr Lys Cys Gin Leu Arg Lys Gly Gly Trp Gln His Asn
 251 ATTGGAAAAT GTACAAGTGT CAGCTAAGGA AAGGAGGCTG GCAACATAAC
 TAACCTTTA CATGTTACCA GTCGATTCTT TTCCCTCGAC CGTTGTATTG

PstI
 +1 Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala
 301 AGAGAACAGG CCAACCTCAA CTCAAGGACA GAAGAGACTA TAAAATTGTC
 TCTCTTGTC GGTTGGAGTT GAGTTCTGT CTTCTCTGAT ATTTAAACG

PstI
DpnI
BglII
 +1 Ala Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg
 351 TGCAGCACAT TATAATACAG AGATCTGAA AAGTATTGAT AATGAGTGGA
 ACGTCGTGTA ATATTATGTC TCTAGAACTT TTCATAACTA TTACTCACCT

SphI
 +1 Arg Lys Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu
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 CTTTCTGAGT TACGTACGGT GCCCTCCACA CATATCTACA CCCCTCCCTC

NruI
DraI
AccI
 +1 Phe Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
 451 TTTGGAGTCG CGACAAACAC CTTCTTAAA CCTCCATGTG TGTCCGTCTA
 AACACCTCAGC GCTGTTGTG GAAGAAATT GGAGGTACAC ACAGGCAGAT

AccI
 +1 Tyr Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser
 501 CAGATGTGGG GGTTGCTGCA ATAGTGAGGG GCTGCAGTGC ATGAACACCA
 GTCTACACCC CCAACGACGT TATCACTCCC CGACGTCACCG TACTTGTGGT

Ddel

+1 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser

551 GCACGAGCTA CCTCAGCAAG ACgttatttg AAATTACAGT GCCTCTCTCT
CGTGCTCGAT GGAGTCGTTC TGCAATAAAC TTTAATGTCA CGGAGAGAGA

+1 Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg

601 CAAGGCCCCA AACCAGTAAC AATCAGTTT GCCAATCACA CTTCCGTGCG
GTTCCGGGGT TTGGTCATTG TTAGTCAAAA CGGTTAGTGT GAAGGACGGC

+1 Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg

651 ATGCATGTCT AAACCTGGATG TTTACAGACA AGTCATTCC ATTATTAGAC
TACGTACAGA TTGACCTAC AAATGTCTGT TCAAGTAAGG TAATAATCTG

+1 Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys

701 GTTCCCTGCC AGCAACACTA CCACAGTGTG AGGCAGCGAA CAAGACCTGC
CAAGGGACGG TCGTTGTGAT GGTGTACAG TCCGTCGCTT GTTCTGGACG

PstI Ddel

+1 Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala Gln Glu

751 CCCACCAATT ACATGTGGAA TAATCACATC TGCAGATGCC TGGCTCAGGA
GGGTGGTTAA TGTACACCTT ATTAGTGTAG ACGTCTACGG ACCGAGTCCT

+1 Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp Gly Phe His

801 AGATTTTATG TTTCCCTCGG ATGCTGGAGA TGACTCAACA GATGGATTCC
TCTAAAATAC AAAAGGAGCC TACGACCTCT ACTGAGTTGT CTACCTAAGG

+1 His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys

851 ATGACATCTG TGGACCAAAC AAGGAGCTGG ATGAAGAGAC CTGTCAGTGT
TACTGTAGAC ACCTGGTTG TTCCGTCGACC TACTTCTCTG GACAGTCACA

PstI PvuII

+1 Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro His Lys Glu Leu

901 GTCTGCAGAG CGGGGCTTCG GCCTGCCAGC TGTGGACCCC ACAAAAGAACT
CAGACGTCTC GCCCCGAAGC CGGACGGTCG ACACCTGGGG TGTTCTTGA

+1 Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Ser Gln

951 AGACAGAAAC TCATGCCAGT GTGTCTGTAA AAACAAACTC TTCCCCAGCC
TCTGTCTTTG AGTACGGTCA CACAGACATT TTTGTTTGAG AAGGGGTCGG

+1 Glu Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys

1001 AATGTGGGGC CAACCGAGAA TTGATGAAA ACACATGCCA GTGTGTATGT
TTACACCCCCG GTTGGCTCTT AACTACTTT TGTGTACGGT CACACATACA

+1 Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys

1051 AAAAGAACCT GCCCCAGAAA TCAACCCCTA AATCCTGGAA AATGTGCCTG
TTTCTTGGGA CGGGGTCTTT AGTTGGGGAT TTAGGACCTT TTACACGGAC

+1 Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His

1101 TGAATGTACA GAAAGTCCAC AGAAATGCTT GTTAAAGGA AAGAAGTTCC
ACTTACATGT CTTCAAGGTG TCTTTACGAA CAATTTCTT TTCTTCAGG

PvuII

+1 His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys

1151 ACCACCAAAAC ATGCAGCTGT TACAGACGGC CATGTACGAA CCGCCAGAAG
TGGTGGTTTG TACGTGACA ATGTCTGCCG GTACATGCTT GGCGGTCTTC

+1 Ala Cys Glu Pro Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro

1201 GCTTGTGAGC CAGGATTTTC ATATAGTGA GAAAGTGTGTC GTTGTGTCCC
CGAACACTCG GTCCTAAAAG TATATCACTT CTTCACACAG CAACACAGGG

DdeI

EagI

NotI

+1 Pro Ser Tyr Trp Lys Arg Pro Gln Met Ser ***

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STRAIN SHEET

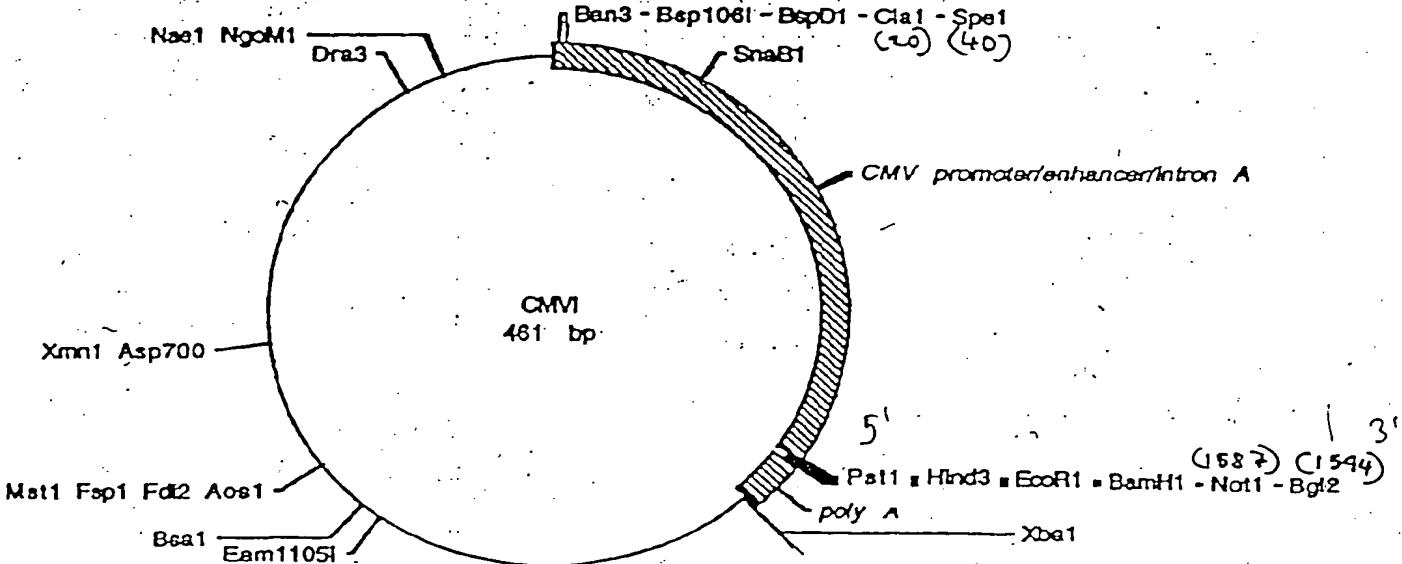
STRAIN CMV I

STORAGE NUMBER 11764

PEDIGREE:

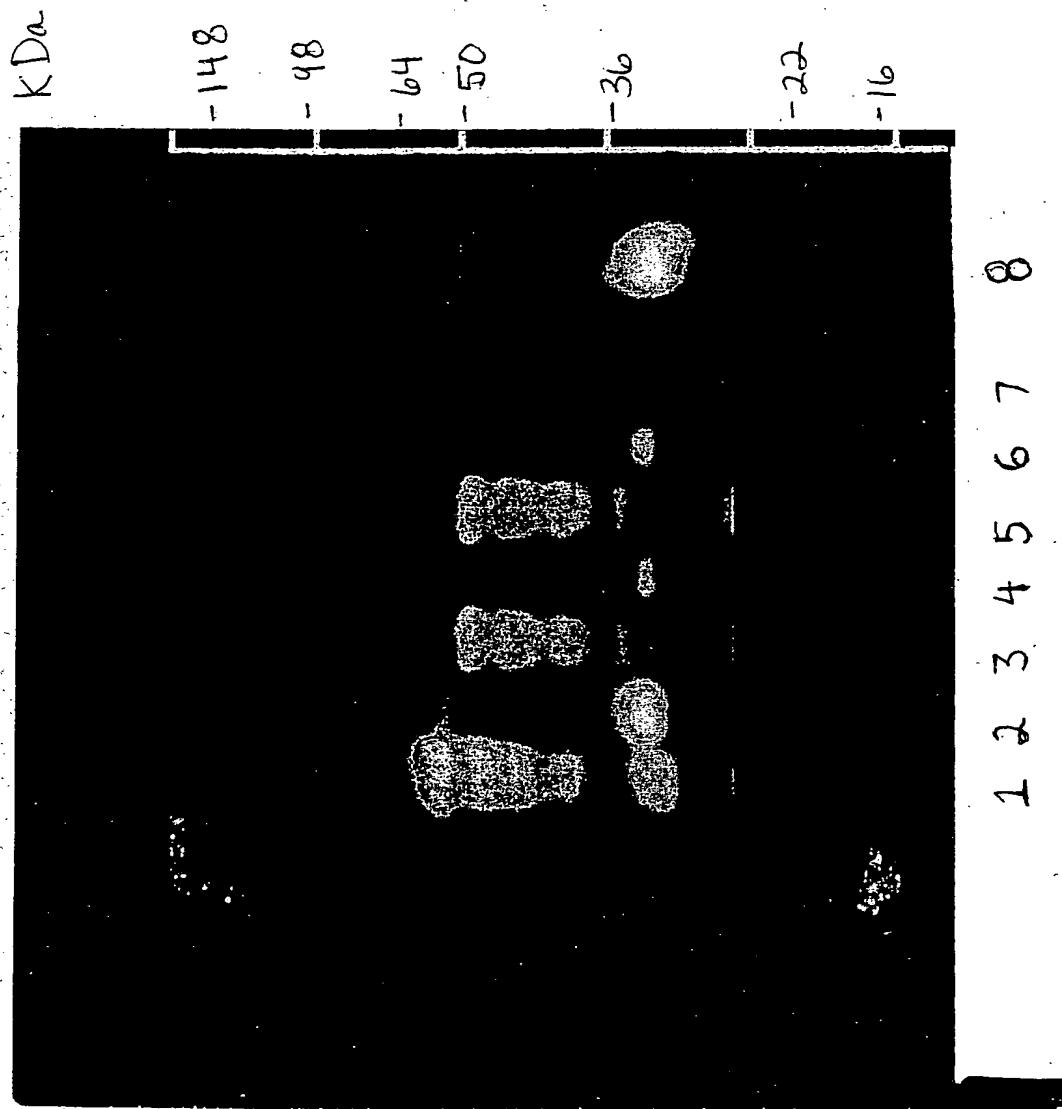
- CMV I was constructed in the pSV7 (nee pSG5 from Stratagene, with an expanded polylinker) backbone by replacing the SV40 promoter from pSV7 with the CMV promoter/enhancer/intron, via 5' Sal I/Xba I (sites destroyed) and 3' Hind III.
- CMV I is 4613 bp.
- CMV I uses ampicillin resistance.
- CMV promoter/enhancer + Intron A: nt 1-1566.
- Polylinker: nt 1566-1597 (5' - Hind III - Eco RI - Bam HI - Not I - Bgl II - 3').
- SV40 polyA addition sequence: nt 1598-1745.
- If for some reason you want to remove the SV40 polyA addition sequence, you can cut with either Sal I or Xba I (these 2 sites border the 3' end of this sequence).

GROWTH REQUIREMENTS:



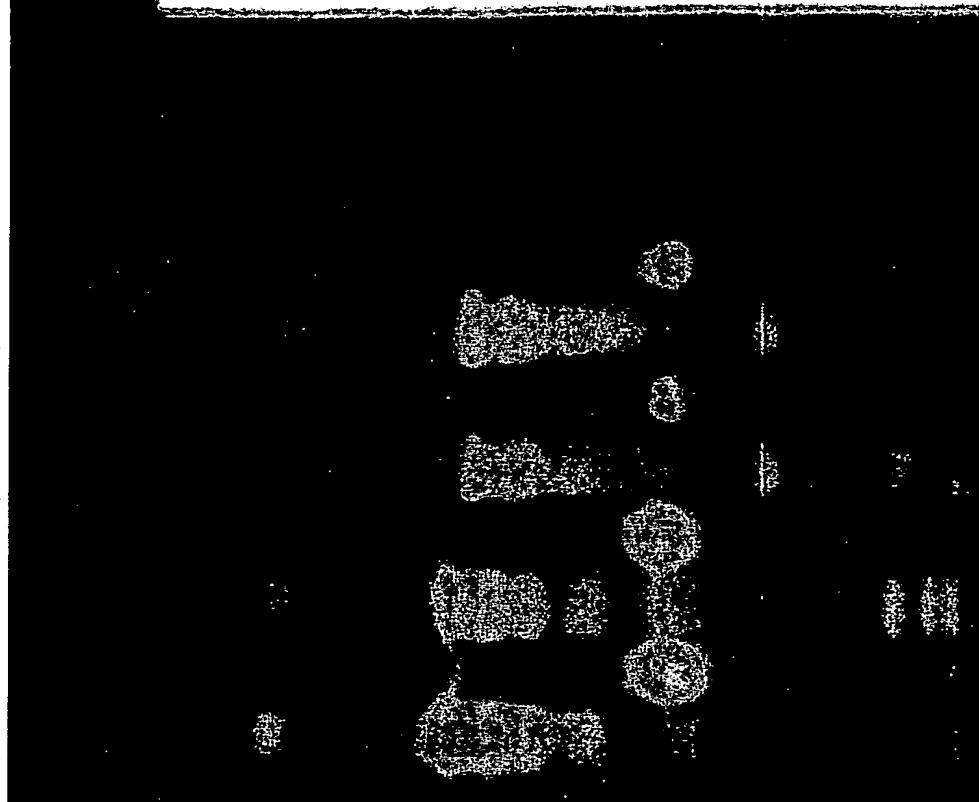
Appendix II

Power Declaration
Figure 1 Gel 1



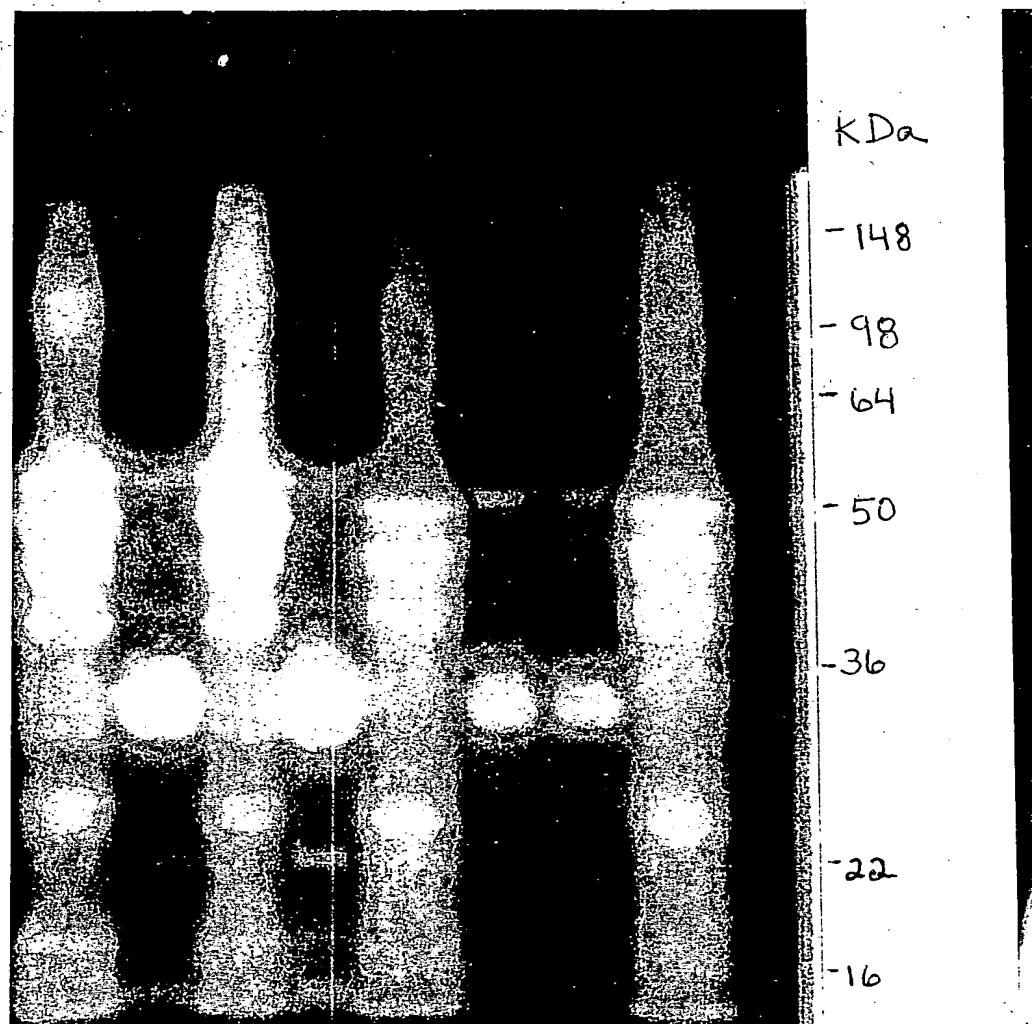
K-Da

-148
-98
-64
-50
-36
-22
-16



9 10 11 12 13 14 15 16 17 18

Power Declaration
Figure 1 - Gel 2



Power Declaration
Figure 1 - Gel 3